

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/508,873A  
Source: PG/10  
Date Processed by STIC: 6/3/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/508,873A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics  
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino  
Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0  
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences  
(OLD RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences  
(NEW RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ **Use of n's or Xaa's  
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>  
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0  
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

## RAW SEQUENCE LISTING

DATE: 06/03/2005

PATENT APPLICATION: US/10/508,873A

TIME: 10:28:53

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06032005\J508873A.raw

IMPORTANT:

see item 4  
on Error Summary  
Sheet  
pp 1-2

2 <110> APPLICANT: TheRyte Ltd.  
W--> 3 <120> TITLE OF INVENTION: Treating Cancer  
W--> 4 <130> FILE REFERENCE: 300051WO Sequence Listing  
W--> 5 <140> CURRENT APPLICATION NUMBER: Not yet known  
C--> 6 <141> CURRENT FILING DATE: 2004-09-23 (this is the U.S. filing date)  
W--> 7 ~~2003-03-25~~  
W--> 8 <150> PRIOR APPLICATION NUMBER:  
W--> 9 0207031.6  
W--> 10 <151> PRIOR FILING DATE:  
W--> 11 2002-03-25  
W--> 12 <150> PRIOR APPLICATION NUMBER:  
W--> 13 0216634.6  
W--> 14 <151> PRIOR FILING DATE:  
W--> 15 2002-07-17  
W--> 16 <150> PRIOR APPLICATION NUMBER:  
W--> 17 0223325.2  
W--> 18 <151> PRIOR FILING DATE:  
W--> 19 2002-10-08  
E--> 20 <160> NUMBER OF SEQ ID NOS:  
W--> 21 4  
24 <170> SOFTWARE: Patentln Ver. 2.1

see item 1  
on Error  
Summary Sheet

Does Not Comply  
Corrected Diskette Needs

The submitted file  
showed a gray grid  
around the <141> through  
the <160> lines. This  
accounts for the "wrapped"  
responses above.

## ERRORED SEQUENCES

26 <210> SEQ ID NO: 1  
27 <211> LENGTH: 18  
28 <212> TYPE: DNA  
29 <213> ORGANISM: Artificial Sequence  
31 <220> FEATURE:  
32 <223> OTHER INFORMATION: Description of Artificial Sequence:  
33 Phosphorothionate oligonucleotide  
35 <220> FEATURE: *use an underscore*  
W--> 36 <221> NAME/KEY: misc\_feature  
37 <222> LOCATION: (1) .. (18)  
38 <223> OTHER INFORMATION: Sense phosphorothionate oligonucleotide having a  
39 sequence identical to a portion of the Rb mRNA  
41 <400> SEQUENCE: 1 (18) *move this to right margin of nucleotide line*  
E--> 42 gtcattgccgc ccaaaacc  
82 <210> SEQ ID NO: 4  
83 <211> LENGTH: 31  
84 <212> TYPE: DNA  
85 <213> ORGANISM: Artificial Sequence

P.2

## RAW SEQUENCE LISTING

DATE: 06/03/2005

PATENT APPLICATION: US/10/508,873A

TIME: 10:28:53

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06032005\J508873A.raw

87 <220> FEATURE:  
88 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide primer  
90 <220> FEATURE:  
91 <221> NAME/KEY: primer\_bind  
92 <222> LOCATION: Complement((1)..(31))  
93 <223> OTHER INFORMATION: Antisense primer comprising a sequence complementary to a  
portion  
94 of the 3' region of the  
97 CDK4 mRNA and the NotI recognition site  
99 <400> SEQUENCE: 4  
100 cccgcggccg ctgctcactc tggattacct t 31

E--> 103 ① delete at end of file

## VERIFICATION SUMMARY

DATE: 06/03/2005

PATENT APPLICATION: US/10/508,873A

TIME: 10:28:54

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\06032005\J508873A.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier  
L:4 M:283 W: Missing Blank Line separator, <130> field identifier  
L:5 M:283 W: Missing Blank Line separator, <140> field identifier  
L:5 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:7 M:259 W: Allowed number of lines exceeded, <141> CURRENT FILING DATE:  
L:8 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:  
L:9 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:  
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:11 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:  
L:12 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:  
L:13 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:  
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:15 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:  
L:16 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:  
L:17 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:  
L:18 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:19 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:  
L:20 M:212 E: (34) Invalid or duplicate Sequence ID Number, Number Of Sequences Unknown  
L:20 M:283 W: Missing Blank Line separator, <160> field identifier  
L:21 M:259 W: Allowed number of lines exceeded, <160> NUMBER OF SEQ ID NOS:  
L:36 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:42 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:1  
L:55 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:103 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:20 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (4)